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expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. bacterial (especially *S. aureus*) infections. They are also useful against *Helicobacter pylori* infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or prognosis a (susceptibility to) disease; for raising antibodies; to identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The MurC gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant MurC gene; for chromosomal mapping; to determine bacterial serotype; and for genetic immunisation.

that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against *S. aureus* infection. The polypeptides can also be used in a kit for the immunodetection of *S. aureus* in a sample. *S. aureus* is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the *S. aureus* DNA sequences contained on the computer readable medium.

Sequence 2424 BP:	839 A:	302 C:	462 G:	759 T:
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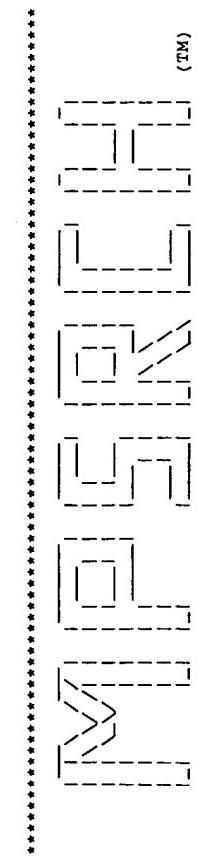


Page 3

polypeptides can also be used in a kit for the immunodetection of *S. aureus* in a sample. *S. aureus* is implicated in numerous human diseases including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scaled skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the *S. aureus* DNA sequences contained on the







Release 3.1A. John F. Collins, Biocomputing Research Unit.  
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**Mpsrch\_tp** n.a. - n.a. Smith-Waterman search, using a protein query which has been backtranslated into n.a. using TOPAC symbols

**Run on:** Sat Nov 27 10:20:03 1999; **Maspar time** 159.66 Seconds

865.603 Million cell updates/sec  
tabular output not generated.

**Title:** >US-09-103-287-4

(1-215) from US09103287.PEP  
**Perfect Score:** 2663

**Description:** 1 TTYAARGAYTWSNGAYGAYAT.....TNGGNATGAAATAAGGNTY 645

AARTTYCTCRWSNCTRCTRA.....ANCCNTACTIYTTRCGNAR

**Scoring table:** TABLE\_bktranslate2  
Gap 3.0

Nmatch STD : Dbase 0; Query 0

Searched: 271905 seqs, 107135622 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

**Database:** n-geneseq35

1:Part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33  
34:part34 35:part35 36:part36 37:part37 38:part38  
39:part39 40:part40 41:part41 42:part42 43:part43  
44:part44 45:part45 46:part46 47:part47 48:part48  
49:part49 50:part50 51:part51 52:part52 53:part53  
54:part54 55:part55 56:part56 57:part57 58:part58  
59:part59 60:part60

**Statistics:**

Mean 50.914; Variance 239.321; scale 0.213

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description	Pred. No.
1	2573	96.6	2424	58	V74703	Staphylococcus aureus
2	2557	96.0	660	60	V80065	Partial nucleotide sequence
3	2329	96.5	1351	60	V99650	UDP-N-acetylglucosamine
c 4	2329	87.5	619	48	V53479	DNA encoding a Staphylococcus faecalis
c 5	934	35.1	677	60	X13717	Enterococcus faecalis
c 6	749	28.1	1267	46	V27381	Streptococcus pneumoniae
c 7	749	28.1	11864	47	V52194	Streptococcus pneumoniae
c 8	699	26.2	1825	47	V43027	Streptococcus pneumoniae

#### ALIGNMENTS

9	222	8.3	861	30	T77403	H. pylori cytoplasmic
10	202	7.6	1365	30	T67723	H. pylori cytoplasmic
11	12	183	6.9	843	47	H. pylori cytoplasmic
c	13	183	6.9	1003	46	Streptococcus pneumoniae
c	14	183	6.9	1350	36	Streptococcus pneumoniae
c	15	183	6.9	1350	52	S. pneumoniae Murd MR
c	16	183	6.9	1353	52	S. pneumoniae Murd ge
c	17	183	6.9	6217	50	DNA encoding S. pneumoniae
c	18	183	6.9	6693	47	Streptococcus pneumoniae
c	19	152	5.7	534	52	Degenerate nucleotide sequence
c	20	151	5.7	1532	47	Synthetic HIV gag gene
c	21	140	5.3	501	3	Sequence encoding new
c	22	140	5.3	1311	59	Degenerate human tumor gene
c	23	141	5.3	1311	59	Human gelosin gene c
c	24	138	5.2	8247	2	Sequence encoding N-t
c	25	139	5.2	1026	30	H. pylori cytoplasmic
c	26	135	5.1	1071	48	Pseudomonas fluorescens
c	27	135	5.1	1782	1	Heat shock protein (H
c	28	137	5.1	003856		Sequence encoding new
c	29	133	5.0	501	3	Degenerate Alteromonas
c	30	134	5.0	510	42	Human interleukin-XX
c	31	134	5.0	984	17	Sequence encoding mat
c	32	132	5.0	1640	2	Gene for human colony
c	33	132	5.0	1641	17	Enterococcus faecalis
c	34	132	5.0	1641	60	Sequence of a cDNA en
c	35	132	5.0	1642	2	Colony stimulating fa
c	36	132	5.0	1642	1	Gene for human colony
c	37	132	5.0	1642	37	Enterococcus faecalis
c	38	132	5.0	1642	33	Human colony stimulat
c	39	132	5.0	1642	26	Human short form CSF-
c	40	132	5.0	1880	46	Arabidopsis thaliana
c	41	132	5.0	2302	35	Human colony stimulat
c	42	132	5.0	2309	13	Partial PCR fragment
c	43	132	5.0	2500	7	Sequence of clone 1am
c	44	132	5.0	4315	60	Enterococcus faecalis
c	45	134	5.0	9767	60	Enterococcus faecalis

RESULT	1	1	standard; DNA; 2424 BP.
ID	V74703	1	
AC	V74703;	1	
DT	16-MAR-1999	1	(first entry)
DE	Staphylococcus aureus conig SEQ ID #392.		
KW	Computer readable medium; vaccine; S. aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; ostomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.		
OS	Staphylococcus aureus.		
FT	misc_feature		
FT	Location/Qualifiers		
FT	1141..12000		
FT	/tag^a		
FT	/note- "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"		

EP-786519-A2.  
PN EP-786519-A2.  
PD 30-JUL-1997.  
PF 07-JAN-1997; 100117.  
PR 05-JAN-1996; US-009861.  
PA (HOMA-) HUMAN GENOME SCI INC.

PI Barash SC, Choi GH, Dillon PJ, Fannin MR, Kunsch CA,  
DR WP.; 97-37432/35.  
PT Polynucleotide(s) and proteins derived from Staphylococcus aureus - stored on computer readable medium and used in the production of anti-S. aureus vaccines  
PT Claim 1; Page 1287-1288; 3271pp; English.  
PS This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access







Q P H T F S R T Q A F L N E F F A E S L C  
 G A D C V Y L C D I F G S A R E N A G K  
 Db 1081 GGNCNGAYTGTNTAYTNTGGAATHTYGGWSNGCNGNRRAGAANGCGNNAR 1140  
 Dt 1102 AAGCAGTCGTCTATTGTTGCAATTGGCTTAATGAGAAATCTGGGCA 1161  
 Qt K A D R V F L C E I F G S I R E N S G A  
 Db L T I G D L Q G K I H N A K L I E E D D  
 Dt 1141 YTNCNGAYTGTNTAYTNTGGAATHTYGGWSNGCNGNRRAGAANGCGNNAR 1200  
 Qt 1162 TTAAGGATAAGGATTAATTGATAATGGGGTGCATTCATTAATGAGATTT 1221  
 Db T S V L K A H D K A V L I F M G A G D I  
 Dt 1201 ACNCNGAYTGTNTAYTCAAGGATGTTGCAATTGGGGCNGNGAYATH 1260  
 Qt 1222 ATTATGTTAGAACATTGATGATGTTGCTTGTCTTGTCTTGTCTTGTCTT 1281  
 Db Q K  
 Dt 1261 CARAART 1267  
 Qt 1282 CAAAAT 1288

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 ID MURC\_PORG1 STANDARD; PRT; 433 AA.

AC 051831;  
 DT 15-JUL-1998 (REL. 36, CREATED)  
 DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)  
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)  
 DE UDP-N-ACETYLUMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-  
 DE ACETYLUMURANOYL-L-ALANINE SYNTHETASE).  
 DE MURC.  
 OS PORPHYROMONAS GINGIVALIS (BACTEROIDES GINGIVALIS).  
 OC BACTERIA; CYTOPHAGALES; BACTEROIDACEAE; PORPHYROMONAS.  
 RN SEQUENCE FROM N.A.  
 RN STRAIN# 381;

RC MEDLINE; 96110684.  
 RX RA ANSAI T., YAMASHITA Y., AWANO S., SHIRATA Y., WACHI M., NAGAI K.,  
 RA TAKEFARA T.;  
 RT "A murC gene in Porphyromonas gingivalis 381.";  
 RL MICROBIOLOGY 141:2047-2052(1995).  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE; 97061201.  
 RX RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMI TZU E., NAKAMURA Y.,  
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,  
 RA HOSODAHI T., MATSUO A., MORAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,  
 RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,  
 RA TABATA S.;  
 RT "Sequence analysis of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions."  
 RT RN SEQUENCE FROM N.A.  
 RT MEDLINE; 97061201.  
 RL DNA RES. 3:109-136(1996).  
 CC -1- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLUMURAMOYL-L-ALANINE -  
 CC ADP + ORTHOPHOSPHATE + UDP-N-ACETYLUMURAMOYL-L-ALANINE.  
 CC -1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE MURDEF FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC -1- DR EMBL; D90916; GI653723;  
 CC KW PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;  
 CC KW ATP-BINDING;  
 CC FT 170 ATP (POTENTIAL);  
 CC NP\_BIND 114 MW; B3D7FC7C CRC32;  
 CC SQ 505 AA; 54513 MW;  
 CC SEQUENCE 433 AA; 48309 MW; 384714B CRC32;  
 CC Score 310; DB 1; Length 433;

Best Local Similarity 40.5%; Pred. No. 8.29e-24;  
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 Qt V I V D D Y A H H P R E I S A T I D T A  
 Db R E I Y S G K H I M G I F Q P H L Y S R  
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 Qt T Q A F L N E F A E S L C K A D R V F L  
 Db L D I  
 Dt 1153 YTNGAYATH 1162  
 Qt 1123 FGTRGTTT 1132  
 Qt C E I

RESULT 4  
 ID MURC\_SYN3 STANDARD; PRT; 505 AA.  
 AC P74526; 1998 (REL. 36, CREATED)  
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)  
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
 DE UDP-N-ACETYLUMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-  
 DE ACETYLUMURANOYL-L-ALANINE SYNTHETASE).  
 DE MURC OR SIR423.  
 OS SYNECHOCYSTIS SP. (STRAIN PCC 6803)  
 OC BACTERIA; CYANOBACTERIA; CHROOCOCcales; SYNECHOCYSTIS.  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RN RP  
 RX MEDLINE; 97061201.  
 RX RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMI TZU E., NAKAMURA Y.,  
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,  
 RA HOSODAHI T., MATSUO A., MORAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,  
 RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,  
 RA TABATA S.;  
 RT "Sequence analysis of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions."  
 RT RN SEQUENCE FROM N.A.  
 RT MEDLINE; 97061201.  
 RL DNA RES. 3:109-136(1996).  
 CC -1- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLUMURAMOYL-L-ALANINE.  
 CC ADP + ORTHOPHOSPHATE + UDP-N-ACETYLUMURAMOYL-L-ALANINE.  
 CC -1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE MURDEF FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC -1- DR EMBL; D90916; GI653723;  
 CC KW PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;  
 CC KW ATP-BINDING;  
 CC FT 164 ATP (POTENTIAL);  
 CC NP\_BIND 505 AA; 54513 MW;  
 CC SEQUENCE 433 AA; 48309 MW; 384714B CRC32;  
 CC Score 309; DB 1; Length 505;  
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#cross-references MUID:98044033  
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 #status translation not shown

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 PID:g263463  
 ##experimental\_source strain 168  
 REFERENCE S71000  
 #authors Varon, D.; Brody, M.S.; Price, C.W.  
 #journal Mol. Microbiol. (1996) 20:339-350.  
 #title Bacillus subtilis operon under the dual control of the general stress transcription factor sigma(B) and the sporulation transcription factor sigma(H).  
 #cross-references MUID:96310371  
 #molecule-type DNA  
 ##residues 85-432 #label VAR  
 ##cross-references EMBL:U31845; NID:9556013; PID:9556014  
 ##experimental\_source strain 168, substrate Marburg  
 GENETICS murC  
 FUNCTION peptidoglycan biosynthesis  
 #pathway ATP binding; cell division; cell wall; ligase; peptidoglycan biosynthesis  
 KEYWORDS #length 432 #molecular-weight 48364 #checksum 6127  
 SUMMARY #length 432 #molecular-weight 48364 #checksum 6127

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 QY 61 DMVYLGQNAFASHEEIVRAHQQLDKVSYNDFLGQIIDOTYSTAVTAGHKGKSTTGLI 120  
 Db 121 HVIQNAKPTSFLLGPGTQGOGENNSEYVFPEACEYRRHFLSYQPDYAIMTMNIDFDHPDXFS 180  
 QY 121 HVMNGDKKTSFLIGDTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTMNIDFDHPDFK 180  
 Db 181 SIDDVDAFEMALQVNKGIIACGCDDEHLPKHANVPVVYGTGEENDQARIVVKSPREG 240  
 QY 181 DINDVDAFQEMAHNVKKGIIAWGDDEHLRKIEADPVYYGFSITDHALYQAQNQITDKG 240  
 Db 241 TFDVDFVRNTFYDIFYIPAYGHHRNLNSLAVIALCHYEEDSSTIKHALKSFGGVKRFN 300  
 QY 241 TAFDVGDFQVLLDDYAHHPTEKVTEAARQKYDPRBIVAFQPFHTTRTOQELDEAESL 300  
 Db 301 EKQLGDQVLLDDYAHHPRENTIDLOGTHNAKLIEDDTSLUKAHDKVLFMAGDI 420  
 QY 301 ETIANQVVDYAHHPREISATIDTARKKYPKEVVAEQPHTESRQAFNEAESLC 360  
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 QY 421 QKLQNAY 427

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 TITLE  
 ORGANISM  
 DATE 08-May-1998 #sequence\_revision 08-May-1998 #text\_change  
 ACCESSIONS B70418

REFERENCE A70300 Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lano, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Auiay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.  
 #journal Nature (1998) 392:353-358  
 #title The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 #cross-references MUID:98196666  
 #accession B70418  
 #status preliminary; nucleic acid sequence not shown;  
 #molecule-type DNA  
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 ##cross-references GB:AB00736; NID:92983763; PID:92983764; GB:AE000657  
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 #gene CLASSIFICATION #superfamily UDP-N-acetylumuramate--alanine ligase  
 #length 454 #molecular-weight 50893 #checksum 2346  
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 Best Local Similarity 30.8%; Pred. No. 2.69e-77;  
 Matches 139; Conservative 125; Mismatches 164; Indels 24; Gaps 20;  
 Db 6 IKKPHFIGGGIGMGSGIAQILLEGYKVGSDDISENKNNTKL-LKQKGAKIYIGHRPENIG 64  
 QY 1 MTHYHFVGIKGGMSSLAQIMHDGHEVQGSDIENYVFTEVALRKNGKTI-LPFGANNIK 59  
 Db 65 DAQVYVSSAVKPNPNEQTAKEKRNNTILPFSKQIAGRELLSEADESDGSFLKLQPAVAVITYNDK 124  
 QY 60 EDMVYIQQAFASHEEIVRAHQQLDKVSYNDFLGQIIDQTSVAVTGAHKTSSTGGL 119  
 Db 125 AEIINAGLEPTVIGGRKLQRTNAKLRGELLYSEADESDGSFLKLQPAVAVITYNDK 184  
 QY 120 SHV NGDKKTSFLIGD---GTGMGLEFSDFAFACEYRRHFLSYKPDYAIMTMNIDF 173  
 Db 185 EHLDYFENFERVKAFAEQMNSVPEYFQAVNNLDDPTLAQVKKSHERVITYGINSPLV 244  
 QY 174 DHPDFKDNDFDQFAQENAHNVYK-GI-TANGDDEHLRK-IE-ADPYIYYGFKDSDDI 229  
 Db 245 RAKNLYLKEGRYERGVFGKKGELGRHIGJIA-GIHNWVYNALAATGVA-LE-LGVVSFEVIR 301  
 QY 230 YAONQITKGTAFDVYDGEF1DHF-LSPOYSDHTVLNALAVIAISYLEKLDTV-N-IK 286  
 Db 302 KSLBEERNAERLLEFLKGTYKNSPVDYDGGHPTEIKAVTINSRLDMYDPKNNLVFOPHRY 361  
 QY 287 EALETFGGYKRRFNETTI-ANQVIVDDAHHPREISATIDTARKYPKEVVAEQPHTF 345  
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 QY 346 SRTOAFLNFAESLCKADRVFLCEIFGSRENSGLATQBLDKIGGASF1-N-EDLIN- 402  
 Db 421 VREYHDEGVILFVGAGTSGKSCBWFKEVNL 452  
 QY 403 VLEQFDNA-VVLFMAGDQDQKLQNAVYLDKLGM 433

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 ENTRY probable UDP-N-acetylumuramate--alanine ligase (murC)  
 TITLE  
 ORGANISM #formal\_name spirochete  
 DATE 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change  
 ACCESSIONS C71338  
 REFERENCE A71250  
 #authors Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwynn, M.; Hickey, E.K.; Clayton, R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod, M.P.; Salzberg, S.; Peterson, J.; Khalil, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDonald,

2 TTTAAAGATTGGATGACATTATGTCTCAAATTCGATAAAGTACTGCT 61  
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 RN [1] RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 98048477.  
 RA LAPITS A., GALLERON N., SOROKIN A., EHRLICH S.D.;  
 RT Sequencing and functional annotation of the *Bacillus subtilis* genes  
 In the 200 kb rRNA-dnaB region.";  
 RL MICROBIOLOGY 143:3431-3441(1997).  
 RN [2] RN  
 RP SEQUENCE OF 85-432 FROM N.A.  
 STRAT=168 / MARBURG;  
 RX MEDLINE; 96310371.  
 RA VARON D., BRODY M.S., PRICE C.W.;  
 RT "Bacillus subtilis operon under the dual control of the general  
 stress transcription factor sigma B and the sporulation transcription  
 factor sigma H.";  
 RL J MOLECULAR MICROBIOLOGY 20:339-350(1996).  
 CC -I- FUNCTION: CELL WALL FORMATION.  
 CC -I- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLGLUCOSAMINOYL + L-ALANINE =  
 CC ADP + ORTHOPHOSPHATE + UDP-N-ACETYLGLUCOSAMINOYL-L-ALANINE.  
 CC -I- PATHWAY: PEPTIDOLYCAN BIOSYNTHESIS.  
 CC -I- SUBCELLULAR LOCATION: PEPTIDOLYCAN.  
 CC -I- SIMILARITY: BELONGS TO THE MURDEF FAMILY.  
 CC DR EMBL: AF008220; G2293216; -.  
 DR EMBL: L31845; G556014; -.  
 DR SUBLIST: BG10973; MURC.  
 KW PEPTIDOLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;  
 FT ATP-BINDING.  
 SQ 108 114 ATP (POTENTIAL)  
 SEQUENCE 432 AA: 48364 MW: 163166CB CRC22;

Query Match Score 40.1%; Best Local Similarity 45.7%; Pred. No. 3.53e-217; Matches 269; Conservative 122; Mismatches 197; Indels 0; Gaps 0;

Db 680 D F Q A R N I V K S T E G T T F D V F V  
 Dt 15 ATGACATTATGGCTAAATTCAAACTGATAAAAGTACTGCCTGATGTG 739  
 Qt D I Y A Q I F Q I T D K G T A V D V Y V  
 Db 740 R N T F Y D T F Y I P A Y G H H N V L N  
 Dt 75 TGGATGGTGGTTATGACTACCTCCCTCCAAATGGACCATACAGTTAA 799  
 Qt D G E F Y D H F L S P Q Y G D H T V L N  
 Db 800 AYWSNTNGNTNATHGNNNTGNYCAYTAYGARGARATHGAYWSNNNTATHAAC  
 Dt 135 ATGCAATTAGGTATTGGCTAAATTAGAGAAAGTGTGATGTGTTAA 134  
 Qt A L A V I A I S Y L E K L D V T N I K E  
 Db 860 AYGNNTNARWSNTTYGGNGNTNAAARMNGNTTAAAGGARAARCGTNGNGAYC 919  
 Dt 195 AAGCATAGAACGTTGGGTAAAGTCGTTCAATGAACTATGCAATC 254  
 Qt A L E T F G V K R R F N E T T I A N Q  
 Db 920 ARGNTNTNATHGAYTAYGCNACAGNCAGTAAARTGAAAGTGTGATGTGTTAA 979  
 Qt L Q N A Y L D K L G M K N A F  
 DE UDP-N-ACETYLGLUCOSAMINOYL-L-ALANINE SYNTHETASE.

RESULT 2  
 ID MURC-BACSU STANDARD: PRT; 432 AA.  
 AC P40778; 01-FEB-1995 (REL. 31, CREATED)  
 DT 36, LAST UPDATE)  
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)  
 DE UDP-N-ACETYLGLUCOSAMINOYL-L-ALANINE SYNTHETASE.

QY	255	AAAGTATTGAGATGATTGCAACCATCAGAGAAATTAGCTCACATTCACAG 314	CC	DR EMBL: D84504; D1025270; -	
QT	256	PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;	KW	PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;	
DB	980	CNMGNCARAAARTAYCNGAAYNGNARATHGTNGCNGTNITYCARCCNCAYACTYACNM 1039	KW	PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;	
DT	980	ATP-BINDING. ATP (POTENTIAL).	KW	PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;	
SEQUENCE	433 AA;	48309 MW;	ATP	ATP-BINDING. ATP (POTENTIAL).	
QY	315	CAGCAAAGAAATACACACAAAGAAATTGCAACATTCACACACTCTCTA 374	9.4%;	Score 310; DB 1; Length 433;	
QT	R K Y P H K E V V A V F Q P H T F S R	Best Local Similarity 40.3%;	Pred. No. 1.10e-24;	Score 310; DB 1; Length 433;	
QT	T Q A F L N E F A E S L K	Matches 77; Conservative 38; Mismatches 75; Indels 0;	Gaps 0;	Best Local Similarity 40.3%;	
DB	1040	GNACNGCARNARTTYINGCARTTYGCGNARWSNTNWNSGNGCNGATGYGNTAY 1099	Db	DR V L I D A H H P V E L D A A I R S V	
DT	1040	GTNTYIATHAYGATGTTGCACTGCGTATTCAGTATTCAGACACTCTCTA 1032	Dt	973 GTNTYIATHAYGATGTTGCACTGCGTATTCAGTATTCAGACACTCTCTA 1032	
QY	375	GAACAAAGAACTTTAAATAAAGAAAGTGGATTTGCAACATTCAGATCTTATTCT 434	Qy	257 GTTATGTTGATGTTGATGTTGCACTTACAGAGAAATTAGTGCTACATGACAGCA 316	
QT	T Q A F L N E F A E S L K	V I V D D Y A H H P E I S A T I D T A	V I V D D Y A H H P E I S A T I D T A		
DB	1100	TNTGIGAYAHTTYYGNNWSNCNMGNGARAYGCNGNAAARYTNACTNCAATHGGNGAYTNC 1159	Db	DR R E I Y S G K H I M G I F Q P H L Y S R	
DT	1100	TATGTAATAATTTGATCAATTAGAGAAATACTCGGCATTAACGATCAAGATTAA 494	Dt	1033 MGNGARATHAYGATGTTGCACTGCGTATTCAGTATTCAGACACTCTCTA 1092	
QY	435	C E I F P G S T R E N T G A L T I Q D L I	Qy	317 CGAAAAATCCACATAAGAAACTGTTGCACTTAAACCACACATTCCTCTAGA 376	
QT	G K I H N A K L I E E D D T S V L K A H	R K K Y P H K E V V A V F Q P H T F S R	R K K Y P H K E V V A V F Q P H T F S R		
DB	1160	ARGNNAAARTHAYAAYGNCNARYTNAATHGARGARGAYGAYACNSNGNTNTAARGCNC 1219	Db	DR T A D F Y Q D F A K S L S M L D Q V V L	
DT	1160	495 TRGATAAAATGGAAGTGGCATCTTATTATGAGATCTTATGAGAACAT 554	Dt	1093 ACNGCNGAYTYYTACGAYTYYCNCNAARWSNTNNTGTYNGAYGRTGNTNTYN 1152	
QY	495	QT Q A F L N E F A E S L K A D R V F L	Qy	377 ACACAGCACTTTAAATGAAAGTTGAGAAGTTAACTGAAAGCATCTGTANTCTA 436	
QT	D K I E G A S L I N E D S I N V L E Q F	QT Q A F L N E F A E S L K A D R V F L	QT Q A F L N E F A E S L K A D R V F L		
RESULT	3	RESULT	4	RESULT	
ID	MURC_PORGI	ID	MURC_ECOLI	ID	MURC_ECOLI
STANDARD;	PRT;	STANDARD;	PRT;	STANDARD;	PRT;
PR	433 AA.	PR	491 AA.	PR	491 AA.
AC	Q51831;	AC	P17952;	AC	P17952;
DT	15-JUL-1998 (REL. 36, CREATED)	DT	007099;	DT	007099;
DT	15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)	DT	16, CREATED)	DT	16, CREATED)
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)	DT	01-AUG-1991 (REL. 16, LAST SEQUENCE UPDATE)	DT	01-AUG-1991 (REL. 16, LAST SEQUENCE UPDATE)
DE	UDP-N-ACETYLUMAMATE ALANINE LIGASE (EC 6.3.2.8) (UDP-N-	DE	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)	DE	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GN	MURC.	DE	DE	DE	DE
OS	PORPHYROMONAS GINGIVALIS (BACTERIOIDES GINGIVALIS).	GN	ACETYLUMANOYL-L-ALANINE SYNTHETASE).	GN	ACETYLUMANOYL-L-ALANINE SYNTHETASE).
OC	BACTERIA; CYTOPHAGALES; BACTEROIDACEAE; PORPHYROMONAS.	OS	MURC.	OS	MURC.
OC	ESCHERICHIA COLI.	OC	ESCHERICHIA COLI.	OC	ESCHERICHIA COLI.
ESCHERICHIA	SEQUENCE FROM N.A.	ESCHERICHIA	SEQUENCE FROM N.A.	ESCHERICHIA	SEQUENCE FROM N.A.
RC	[1]	RC	STRAIN=K12;	RC	STRAIN=K12;
RC	SEQUENCE FROM N.A.	RC	STRAIN=K12;	RC	STRAIN=K12;
RX		RX	MEDLINE; 92326550.	RX	MEDLINE; 92326550.
RA	ANSAI T., YAMASHITA Y., AWANO S., SHIBATA Y., WACHI M., NAGAI K.,	RA	IKEDA M., WACHI M., JUNG H.K., ISHINO F., MATSUHASHI M.;	RA	IKEDA M., WACHI M., JUNG H.K., ISHINO F., MATSUHASHI M.;
RA	TAKEHARA T.;	RT	"A murc gene in Porphyromonas gingivalis 381."	RT	"Nucleotide sequence involving murc and murC in the mra gene cluster
RT	RT	DE	DE	DE	DE
DE	MICROBIOLOGY 141:2047-2052(1995).	DE	ACETYLUMANOYL-L-ALANINE SYNTHETASE).	DE	ACETYLUMANOYL-L-ALANINE SYNTHETASE).
RL	[2]	RT	region of Escherichia coli."	RT	region of Escherichia coli."
RN	REVISIONS.	RL	NUCLEIC ACIDS RES. 18:4014-4014(1990).	RL	NUCLEIC ACIDS RES. 18:4014-4014(1990).
RP	STRAIN=381;	RN	[2]	RN	[2]
RC		RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RC		RN	STRAIN=K12 / MG1655;	RC	STRAIN=K12 / MG1655;
RC		RN	MEDLINE; 92326617.	RC	MEDLINE; 92326617.
CC	SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.	CC	BLATTNER F., PLUNKETT G. III., BLOCH C.A., PERNA N.T., BURLAND V.,	CC	BLATTNER F., PLUNKETT G. III., BLOCH C.A., PERNA N.T., BURLAND V.,
CC	-!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).	CC	YORA T., MORI H., NAGAI H., NAGATA T., ISHIHAMA A., FUJITA N.,	CC	YORA T., MORI H., NAGAI H., NAGATA T., ISHIHAMA A., FUJITA N.,
CC	-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLUMANOYL + L-ALANINE -	CC	RA	RA	RA
CC	ADP + ORTHOPHOSPHATE + UDP-N-ACETYLUMANOYL-L-ALANINE.	CC	RA	RA	RA
CC	-!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.	CC	RA	RA	RA
CC	-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).	CC	RT	RT	RT
CC	-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.	CC	RT	RT	RT
CC	[3]	CC	THE 0-2'-mim region.	RL	THE 0-2'-mim region.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	CC	NUCLEIC ACIDS RES. 20:3305-3308(1992).	RL	NUCLEIC ACIDS RES. 20:3305-3308(1992).
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	CC	[3]	RN	[3]
CC	the European Bioinformatics Institute. There are no restrictions on its	CC	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
CC	use by non-profit institutions as long as its content is in no way	CC	STRAIN=K12 / MG1655;	RC	STRAIN=K12 / MG1655;
CC	modified and this statement is not removed. Usage by and for commercial	CC	MEDLINE; 92326617.	RC	MEDLINE; 92326617.
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>	CC		RA	
CC	or send an email to license@isb-sib.ch).	CC		RA	



/protein_id="AAB40046_1"	Bron,S., Brouillet,S., Bruschi,C.V., Caldwell,B., Capuano,V., Carter,N.M., Choi,S.K., Codani,J.F., Connerton,I.F., Cummings,N.J., Daniel,R.A., Denizot,F., Devine,K.M., Dusterhoff,A., Ehrlich,S.D., Emmerson,P.T., Entian,K.D., Errington,J., Fabre,C., Ferrari,E., Fouliger,D., Fritz,C., Fujita,M., Fujita,Y., Fuma,S., Galizzi,A., Galleron,N., Ghim,S.Y., Glaser,P., Goffeau,A., Golightly,E.J., Grandi,G., Guiseppi,G., Guy,B.J., Haga,K., Hailech,J., Harwood,C.R., Henaut,A., Hilbert,H., Holzapfel,S., Hosono,S., Hullu,M.F., Itaya,M., Jones,L., Joris,B., Karamata,D., Kasahara,Y., Klaerr-Blanchard,M., Klein,C., Kobayashi,Y., Koetter,P., Konigstein,G., Krogh,S., Kurama,M., Kurita,K., Lapidus,A., Lardinois,S., Lauber,J., Lazarevic,V., Lee,S.M., Meliado,R.P., Masuda,S., Mauli,C., Medigue,C., Medina,N., Nonne,D., O'Reilly,M., Mizuno,M., Moestl,D., Nakai,S., Noback,M., Park,S.H., Parro,V., Pohl,T.M., Portetelle,D., Porwollik,S., Prescott,A.M., Pujoic,P., Purnelle,B., Rapoport,G., Rey,M., Reynolds,S., Rieger,M., Rivolta,C., Roche,B., Rose,M., Sadaie,Y., Sato,T., Scanlan,E., Schleich,S., Schroeter,R., Scoffone,F., Sekiguchi,J., Sokorska,A., Seror,S.J., Servar,P., Shin,B.S., Sojdo,B., Sorokin,A., Tacconi,B., Takagi,T., Takahashi,H., Takemaru,K., Takeuchi,M., Tamakoshi,A., Tanaka,T., Terpstra,P., Tonnon,A., Tosato,V., Uchiyama,S., Vandembol,M., Vannier,F., Vassarotti,A., Viari,A., Wambutt,R., Wedler,E., Wedler,H., Weitzenecker,T., Winters,P., Wipat,A., Yamamoto,H., Yamane,K., Yamamoto,K., Yata,K., Yoshida,K., Yoshihara,H.F., Zumstein,E., Yoshihara,H. and Danchin,A.
/db_xref="PID:9556017"	the complete genome sequence of the gram-positive bacterium Bacillus subtilis
/db_xref="GI: 5556017"	Nature 390 (6657), 249-256 (1997)
/translation="MAKQLQSEEEFKRIAEGEVEFLKHSSTTCPISQAFAHEFDFANQHEDPAYL"	JOURNAL 98044033
BASE COUNT	750 a
ORIGIN	464 C
Query Match	49 2%
Best Local Similarity	45 2%
Matches	Pred. No. 3.43e-12;
272; Conservative	Mismatches 207; Indels 0; Gaps 0;
Db 430 ATGATTTCAGGCCAACATGTAAAGACGGAAACCTTGTATGCTTTG 489	Scallop, E., Schleich,S., Schroeter,R., Scoffone,F., Sekiguchi,J., Scanlan,E., Serror,P., Shin,B.S., Sojdo,B., Sorokina,A., Seror,S.J., Servar,P., Shin,B.S., Shin,B.S., Soido,B., Sorokin,A., Tacconi,B., Takagi,T., Takahashi,H., Takemaru,K., Takeuchi,M., Tamakoshi,A., Tanaka,T., Terpstra,P., Tonnon,A., Tosato,V., Uchiyama,S., Vandembol,M., Vannier,F., Vassarotti,A., Viari,A., Wambutt,R., Wedler,E., Wedler,H., Weitzenecker,T., Winters,P., Wipat,A., Yamamoto,H., Yamane,K., Yamamoto,K., Yata,K., Yoshida,K., Yoshihara,H.F., Zumstein,E., Yoshihara,H. and Danchin,A.
QY 14 AYGAYATHAYGCNCARATHYTICARATHACNGAYAARGGNACNGCNGTNTAYG 73	TITLE
Db 490 TCCGAATACGGTCTATACCTTATATGGCTTATGCCATTAGAAGAAATTGATTGCTTACGCCAACATGTATAAAC 549	JOURNAL 98044033
QY 74 TNGAYGGGAGTYYTAIGCAWTTYTNWSNCNCNCAATYNGGAGCAGANGNTNTNA 133	REFERENCE 2 (bases 1 to 215640)
Db 550 ACTCATGGGGCATATGGCTTATGCCATTAGAAGAAATTGATTGCTTACGCCATATAAGC 609	AUTHORS Kunst,F., Ogasawara,N., Yoshihara,H. and Danchin,A.
QY 134 AYGNYTNCNGTNCNATHCNATHSNTAYTNGARAARYTNGAYTGTACNAYATHAARG 193	DIRECT SUBMISSION
Db 610 ATGTCCTCAAATCCTTGGGGTCAACCGAGATCAATAGAAACGAGCTGGGATC 669	JOURNAL Submitted (18 NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45 68 89 48
QY 194 ARGCNNTGARACNTTYGGNGGNTNARMGNNTYYAAYGARACNACTGNCNAYC 253	FEATURES Location/Qualifiers
Db 670 ATGGCTGATTGACTGACTGCCATATGGTACGATGGCAGAAATAAGTACAATCGAGGCCGG 729	1. 215640
QY 254 ARNTNATGTTGAGATAYGGCAYCAYCZCNGNGNARATHNSNGNACNATHAYACNG 313	/organism="Bacillus subtilis"
Db 730 CAGACAGAACTTCTGATGGAAATTGTCGGPATTCAGCCCTCATACATTACCC 789	/strain="168"
QY 314 CNNGNAAARAAARTAYCCNCAYAARGARGTNTGNCNGNTNTYCARNCCNAYACNTTWSNM 373	/db_xref="taxon:1423"
Db 790 GGAGCACGAGCTTCTGAGATTGGAGAAAGCCGAGCTGTGTGTTATT 849	complement(8..1423)
QY 374 GNPNCCARGCNTTYTNTRAYGARTTYGCNGAMSNNTNWNSNARGCNGAYMGNGTNTYY 433	/gene="YntM"
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QY 554 TYRAYAAYGCGNTGNTNTYYTNTAYGARTTYGCNGAMSNNTNWNSNARGCNGAYTNGNARAYTNCARAAYGCNT 613	/function="unknown"
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QY 614 AY 615	/transl_table=11
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LOCUS BSUB0016	/db_xref="PID:e1185101"
DEFINITION Bacillus subtilis complete genome (section 16 of 21): from 2997711	/db_xref="PID:32635412"
VERSION 929119 AL009126	/db_xref="GI:2635412"
VERSION 929119.1 GI:2635411	/SPTRMBL:034430"
KEYWORDS	/translation="MKKLQIPAFIGTSOLIDSIGMAVTSPSILLAFGITEAVAS
ORGANISM Bacillus subtilis	ASVHLAEVTTAASGVSHAFGNDKOTVLPQVSGAFLQGPQDIAKPY
REFERENCE Azedo, V., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Bessieres, P., Bolotin, A., Borchert, S., Brignell, S.C., Borriiss, R., Bourrier, L., Brans, A., Braun, M., Brignell, S.C.,	ISLFLILQGLSPRKVYQGTVDTSEFIAVATAGELISIGKEDVNLWVSLMAGGIIA
AUTHORS	TPILSRKGKLSPRKVYQGTVDTSEFIAVATAGELISIGKEDVNLWVSLMAGGIIA
REFERENCE Azedo, V., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Bessieres, P., Bolotin, A., Borchert, S., Brignell, S.C., Borriiss, R., Bourrier, L., Brans, A., Braun, M., Brignell, S.C.,	LFLVLSIGNRNIVKAVDWHLKEK
REFERENCE Azedo, V., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Bessieres, P., Bolotin, A., Borchert, S., Brignell, S.C., Borriiss, R., Bourrier, L., Brans, A., Braun, M., Brignell, S.C.,	complement(1020..2270)
REFERENCE Azedo, V., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Bessieres, P., Bolotin, A., Borchert, S., Brignell, S.C., Borriiss, R., Bourrier, L., Brans, A., Braun, M., Brignell, S.C.,	/gene="hipo"
REFERENCE Azedo, V., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Bessieres, P., Bolotin, A., Borchert, S., Brignell, S.C., Borriiss, R., Bourrier, L., Brans, A., Braun, M., Brignell, S.C.,	/EC_number="3.5.1.32"
REFERENCE Azedo, V., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Bessieres, P., Bolotin, A., Borchert, S., Brignell, S.C., Borriiss, R., Bourrier, L., Brans, A., Braun, M., Brignell, S.C.,	/product="hippurate hydrolase"
REFERENCE Azedo, V., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Bessieres, P., Bolotin, A., Borchert, S., Brignell, S.C., Borriiss, R., Bourrier, L., Brans, A., Braun, M., Brignell, S.C.,	/protein_id="CAB14907_1"

Qy	61	TNIKAELTEFGGVKRRFNETTIANQVIVDDYAHHPREISATIDTARKYKPHKEVAVFQP	120
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Qy	121	HTFSRTOAFLNEFASSLKADRVECEIFSGIRENTGALTIQDLDKIGASLINE	DSIN 402
Db	403	VLEQFDNAVVLFGAGDIIQKLQNALDKLGKNAF	437
Qy	181	VLEQFDNAVVLFGAGDIIQKLQNALDKLGKNAF	215
RESULT	2		
ID	MORC_BACSU	STANDARD;	PRT;
AC	P40778;		432 AA.
DT	01-FEB-1995 (REL. 31, CREATED)		
DT	15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)		
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)		
DE	UDP-N-ACETYLGLURAMATE-ALANINE LIGASE (EC 6.3.2.8) (UDP-N-		
DE	ACETYLURIDYL-L-ALANINE SYNTHETASE).		
GN	MURC.		
OS	BACILLUS SUBTILIS.		
OC	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 9804467.		
RA	LAPIDUS A., GALLERON N., SOROKIN A., EHLRICH S.D.		
RT	* Sequencing and functional annotation of the <i>Bacillus subtilis</i> genes in the 200 kb rrnB-dnaB region.",		
RT	[JOURNAL] MICROBIOLOGY 143:4331-4441(1997);		
RL	[PUBMED] 91310371.		
RN	[2]		
RP	SEQUENCE OF 85-432 FROM N.A.		
RX	STRAIN=168 / MARBURG.		
RX	MEDLINE; 96310371.		
RA	VARON D., BRODY M.S., PRICE C.W.,		
RT	* <i>Bacillus subtilis</i> operon under the dual control of the general stress transcrption factor sigma B and the sporulation transcription factor sigma H.,		
RN	[3]		
RL	MOL. MICROBIOL. 20:339-350(1999).		
CC	-1 - FUNCTION: CELL WALL FORMATION.		
CC	-1 - CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLGLURAMOYL + L-ALANINE - ADP + ORTHOPHOSPHATE + UDP-N-ACETYLGLURAMOYL-L-ALANINE.		
CC	-1 - PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.		
CC	-1 - SUBCELLULAR LOCATION: CYTOPLASMIC.		
CC	-1 - SIMILARITY: BELONGS TO THE MURDEF FAMILY.		
CC	-1 -		
CC	This SWISS-PROT entry is copyright. It is produced through a collaborative		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a> or send an email to license@isb-sib.ch).		
CC	[4]		
CC	EMBL: AF008220; G229316; -.		
CC	EMBL: L31845; G556014; -.		
CC	SUBMITID: BG10973; MURC.		
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KW	ATP-BINDING.		
NP	NP_BIND 108 114 ATP (POTENTIAL).		
DR	SEQUENCE 432 AA; 48364 MW; 163166CB CRC32;		
Query Match	57.7%	Score 863; DB 1; Length 432;	
Best Local Similarity	59.1%	Pred. No. 1, 20e-32;	
Matches	120; Conservative	Mismatches 51; Indels 0; Gaps 0;	
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b	: :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
b	3 DSDDIYAQFQIDKGTAQVYDVEGFYDHFLSPQGDHTVNLALVIAISYLEKLDTVN	62	
b	285 IKHALKSTGGVKKRBNENKGQVLLDDAHHPTEIKYTERAAQKYPREIVAVFQPIT	344	
b	: :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
63	IKEALETFGGVKRKFNETTIANQVIVDDYAHHPREISATIDTARKYKPHKEVAVFQPIT	122	